



04-18-23

Box seq-

1646

Attorney Docket No. 5470-130DV

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re: French et al.
Serial No.: 09/497,822
Filed: February 3, 2000

Confirmation No. 7943
Group Art Unit: 1646
Examiner: M. Pak

For: ANDROGEN RECEPTOR PROTEINS, RECOMBINANT DNA MOLECULES
CODING FOR SUCH, AND USE OF SUCH COMPOSITIONS

Date: April 16, 2003

BOX SEQUENCE
PO Box 2327
Arlington, VA 22202

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**STATEMENT IN SUPPORT OF FILING A
SEQUENCE LISTING UNDER 37 CFR § 1.821(f)**

Sir:

I hereby state that the content of the paper and computer readable copies of the Sequence listing are the same. I also hereby state as required by 37 CFR § 1.821(h) that the computer readable copy submitted concurrently herewith contains no new matter, nor does it go beyond the disclosure of the application as filed.

Respectfully submitted,

Jarett K. Abramson
Registration No. 47,376



20792

PATENT TRADEMARK OFFICE

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Clara R. Beard



SEQUENCE LISTING

<110> French, Frank
Wilson, Elizabeth
Joseph, David
Lubahn, Dennis

<120> ANDROGEN RECEPTOR PROTEINS RECOMBINANT DNA MOLECULES AND CODING
FOR SUCH AND USE OF SUCH COMPOSITIONS

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<141> 2000-02-03

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<170> PatentIn version 3.1

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Arg	Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	Lys	Ala	Leu	Pro	Gly	Phe	
			695				700					705				
cgc	aac	ttg	cat	gtg	gat	gac	cag	atg	gca	gtc	att	cag	tat	tcc	tgg	3294
Arg	Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	Val	Ile	Gln	Tyr	Ser	Trp	
		710				715					720					
atg	gga	ctg	atg	gta	ttt	gcc	atg	ggc	tgg	cgg	tcc	ttc	act	aat	gtc	3342
Met	Gly	Leu	Met	Val	Phe	Ala	Met	Gly	Trp	Arg	Ser	Phe	Thr	Asn	Val	
					730				735						740	
aac	tct	agg	atg	ctc	tac	ttt	gca	cct	gac	ctg	gtt	ttc	aat	gag	tat	3390
Asn	Ser	Arg	Met	Leu	Tyr	Phe	Ala	Pro	Asp	Leu	Val	Phe	Asn	Glu	Tyr	
				745					750					755		
cgc	atg	cac	aag	tct	cga	atg	tac	agc	cag	tgc	gtg	agg	atg	agg	cac	3438
Arg	Met	His	Lys	Ser	Arg	Met	Tyr	Ser	Gln	Cys	Val	Arg	Met	Arg	His	
			760					765					770			
ctt	tct	caa	gag	ttt	gga	tgg	ctc	cag	ata	acc	ccc	cag	gaa	ttc	ctg	3486
Leu	Ser	Gln	Glu	Phe	Gly	Trp	Leu	Gln	Ile	Thr	Pro	Gln	Glu	Phe	Leu	
		775					780					785				
tgc	atg	aaa	gca	ctg	cta	ctc	ttc	agc	att	att	cca	gtg	gat	ggg	ctg	3534
Cys	Met	Lys	Ala	Leu	Leu	Leu	Phe	Ser	Ile	Ile	Pro	Val	Asp	Gly	Leu	
		790				795					800					

aaa aat caa aaa ttc ttt gat gaa ctt cga atg aac tac atc aag gaa 3582
 Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu
 805 810 815 820

ctt gat cgc atc att gca tgc aaa aga aaa aat ccc aca tcc tgc tca 3630
 Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys Ser
 825 830 835

agg cgc ttc tac cag ctc acc aag ctc ctg gat tct gtg cag cct att 3678
 Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro Ile
 840 845 850

gca aga gag ctg cat caa ttc act ttt gac ctg cta atc aag tcc cat 3726
 Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser His
 855 860 865

atg gtg agc gtg gac ttt cct gaa atg atg gca gag atc atc tct gtg 3774
 Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser Val
 870 875 880

caa gtg ccc aag atc ctt tct ggg aaa gtc aag ccc atc tat ttc cac 3822
 Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe His
 885 890 895 900

aca cag tgaagatttg gaaccttaata cccaaaccca cctgttcctt tttcagatgt 3878
 Thr Gln

cttctgcctg ttatataact ctgcactact tctctggcat gggccttggg ggaaattcct 3938

ctactgatgt acagtctgtc atgaacatgt tccccaagtt ctatttcctg ggcttttcct 3998

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 <213> Rattus rattus

<400> 21

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Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
 20 25 30

Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ile Ala
 35 40 45

Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg
 50 55 60

Arg Arg Arg Gln Gln His Pro Glu Asp Gly Ser Pro Gln Ala His Ile
 65 70 75 80

Arg Gly Thr Thr Gly Tyr Leu Ala Leu Glu Glu Glu Gln Gln Pro Ser
 85 90 95

Gln Gln Gln Ser Ala Ser Glu Gly His Pro Glu Ser Gly Cys Leu Pro
 100 105 110

Glu Pro Gly Ala Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro
 115 120 125

Pro Ala Pro Pro Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser
 130 135 140

Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Ile
 145 150 155 160

Lys Asp Ile Leu Ser Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln
 165 170 175

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 180 185 190

Gln Gln Gln Glu Val Ile Ser Glu Gly Ser Ser Ser Val Arg Ala Arg
 195 200 205

Glu Ala Thr Gly Ala Pro Ser Ser Ser Lys Asp Ser Tyr Leu Gly Gly
 210 215 220

Asn Ser Thr Ile Ser Asp Ser Ala Lys Glu Leu Cys Lys Ala Val Ser
 225 230 235 240

Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly
 245 250 255

Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Ser Leu Leu Gly Gly Pro
 260 265 270

Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys Lys Gly
 275 280 285

Leu Ser Leu Asp Glu Gly Pro Gly Lys Gly Thr Glu Glu Thr Ala Glu
 290 295 300

Tyr Ser Ser Phe Lys Gly Gly Tyr Ala Lys Gly Leu Glu Gly Glu Ser
 305 310 315 320

Leu Gly Cys Ser Gly Ser Ser Glu Ala Gly Ser Ser Gly Thr Leu Glu
 325 330 335

Ile Pro Ser Ser Leu Ser Leu Tyr Lys Ser Gly Ala Val Asp Glu Ala
 340 345 350

Ala Ala Tyr Gln Asn Arg Asp Tyr Tyr Asn Phe Pro Leu Ala Leu Ser
 355 360 365

Gly Pro Pro His Pro Pro Pro Pro Thr His Pro His Ala Arg Ile Lys
 370 375 380

Leu Glu Asn Pro Ser Asp Tyr Gly Ser Ala Trp Ala Ala Ala Ala Ala
 385 390 395 400

Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly Gly Ser Val Ala
 405 410 415

Gly Pro Ser Thr Gly Ser Pro Pro Ala Thr Ala Ser Ser Ser Trp His
 420 425 430

Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Gly Gly Gly
 435 440 445

Gly Gly Ser Ser Ser Pro Ser Asp Ala Gly Pro Val Ala Pro Tyr Gly
 450 455 460

Tyr Thr Arg Pro Pro Gln Gly Leu Ala Ser Gln Glu Gly Asp Phe Ser
 465 470 475 480

Ala Ser Glu Val Trp Tyr Pro Gly Gly Val Val Asn Arg Val Pro Tyr
 485 490 495

Pro Ser Pro Ser Cys Val Lys Ser Glu Met Gly Pro Trp Met Glu Asn
 500 505 510

Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu Asp Ser Thr Arg Asp His
 515 520 525

Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile
 530 535 540

Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly
 545 550 555 560

Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr
 565 570 575

Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys
 580 585 590

Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr
 595 600 605

Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu
 610 615 620

Glu Gly Glu Asn Ser Ser Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln
 625 630 635 640

Lys Met Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe
 645 650 655

Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His
 660 665 670

Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn
 675 680 685

Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala
 690 695 700

Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile
 705 710 715 720

Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser
 725 730 735

Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val
 740 745 750

Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val
 755 760 765

Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro

770

775

780

Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro
785 790 795 800

Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn
805 810 815

Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro
820 825 830

Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser
835 840 845

Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu
850 855 860

Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu
865 870 875 880

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El
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Asp His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr
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